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Trait Reduction in Chickpea (*Cicer arietinum* L.) Germplasm through Principal Component Analysis

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A B S T R A C T

Enhancing chickpea (*Cicer arietinum* L.) seed production can be achieved by selecting superior genotypes according to various yield and yield component characteristics. Yield is a multidimensional feature that is controlled by several circumstances; thus, principal component analysis, a well-established method, was used to discover and limit the number of characteristics necessary for effective selection. As a result, this experiment was conducted to analyze the genetic diversity of chickpea genotypes. The study involved 81 chickpea germplasm lines and 15 check varieties, totalling 96, assessed through an augmented block design with four blocks. Each experimental unit consisted of two rows per genotype, each 2 meters in length, with a 0.5-meter gap between rows and plants spaced 30 × 10 cm apart. Standard procedures were used to obtain data on 10 quantitative traits for every genotype. Among the ten principal components (PCs) analyzed, only three had eigenvalues exceeding 1.0, accounting for approximately 63.97% of the variability. PC 1 accounted for the largest portion of variability at 26.39%. This was followed by PC 2, which explained 21.79% of the variability with an eigenvalue of 2.17, and PC 3, which accounted for 15.79% with an eigenvalue of 1.57. The first three PCs—days to 50% pod setting, days to 50% flowering, and days to maturity—accounted for 63.97% of the overall variation and explained the characteristics. Genotypes frequently appearing in more PCs included ICC-16534, ICC-6816, ICC-12726, and CSJ-515. The current study revealed that chickpea germplasm exhibited significant genetic diversity across most of the traits examined.

Introduction

Chickpea (*Cicer arietinum* L.) (2n=2X=16), belonging to the subfamily Papilionaceae within the family Leguminosae, is a notable and unique food legume (Jain *et al.,* 2022). It is widely grown around the world and is considered the second most significant grain legume crop, following dry beans, in terms of global planting area. Chickpeas play a vital role in farming within dry and semi-dry areas and are also successfully cultivated in winter crop rotations alongside cotton and maize in regions with temperate climates. However, warm and rainy climatic circumstances make Ascochyta blight a significant obstacle to winter-sown chickpea output, leading to considerable yield losses (Ton, 2023). Ensuring food and nutritional security is both economically and ecologically vital, particularly in climates subject to variability. This crop accounts for approximately 12 percent of pulse production worldwide (Mallu *et al.,* 2015). Beyond its nutritional benefits, chickpea enhances soil fertility via symbiotic nitrogen fixation. Lately, chickpea cultivation has expanded to over 50 countries worldwide (Tsehaye *et al.,* 2020). In India, chickpea production is projected to decline by 198 thousand metric tonnes (KMT) to 11.337 million metric tonnes (MMT) by 2025 (The Ministry of Agriculture and Farmers Welfare, 2024). Although states such as Madhya Pradesh, Andhra Pradesh, Maharashtra, and Karnataka have increased their chickpea cultivation areas, the growth of irrigated wheat farming has led to a notable decrease in chickpea cultivation in areas such as Punjab, Haryana, Uttar Pradesh, and Bihar (Arya *et al.,* 2019).

Due to a limited genetic foundation and a variety of biotic and abiotic stressors, chickpea production potential has been severely curtailed. One of the main causes of the drop in chickpea yields per unit area is the limited genetic base and the lack of commercial cultivars with high yields. According to Agrawal *et al.,* (2018), the majority of commercial chickpea cultivars are vulnerable to climate change and show little tolerance for a variety of environmental conditions. Individual variability is necessary for a species to survive in the wild and is a requirement for crop genetic modification initiatives to be effective (Singh *et al.,* 2021). A primary obstacle to utilizing these cultivars has been the lack of knowledge regarding key economic traits (Gaur *et al.,* 2012). Breeders must prioritize adaptation in varietal development initiatives to achieve sustainable agronomic benefits. Enhancing chickpea yield can be accomplished by selecting superior genotypes directly associated with seed yield. Breeding programs can use these genotypes just to increase grain yield. Since yield is a complicated characteristic that is impacted by a variety of environmental factors, principal component analysis, or PCA, has been developed. To cut down on the number of traits needed for effective selection, PCA finds and ranks the most relevant qualities.

Modern data analysis relies heavily on PCA, a simple, non-parametric method for extracting relevant information from mixed datasets. To uncover the sometimes-concealed simplified structure that frequently underpins complicated data collection, PCA offers a path for reducing it to a lower dimension with the least amount of work. It preserves the majority of the dataset's variety while lowering the dimensionality of the data. PCA achieves this reduction by employing a small number of components to find the principal components or directions along which the data variation is maximum; A relatively small amount of numbers, as opposed to values for thousands of variables, can be used to represent each sample. Therefore, measuring the importance of each dimension for describing the variability of a dataset is PCA's primary benefit. Principal components, or a (lower) number of uncorrelated variables, are created by converting several (possibly) linked variables via a mathematical method (Muniraja *et al.,* 2011).

Materials and Methods

Using principal component analysis, this study was conducted in Rabi 2024–2025 at the Student Inspection Farm, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, Uttar Pradesh, to evaluate superior chickpea genotypes.

The materials used in the experiment included 96 distinct genotypes of chickpeas, 15 of which were check varieties (Table 1), evaluated for ten quantitative traits, and sown augmented block design consisting of four blocks. The recommended packages and practices required for healthy crops were also included. The samples were from Hyderabad's International Crop Research Institute for Semi-Arid Tropics (ICRISAT). Two 2.0-meter rows were planted in each block, separated by 30 cm between rows and 8–10 cm between plants. Six quantitative characteristics were documented: days to 50% flowering (DF 50%), days to 50% pod setting (DPS 50%), days to maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPB), number of secondary branches per plant (NPB), number of pods per plant (NPD/P), number of seeds per pod (NSD/PD), 100 seed weight (100 SW), and seed yield per plant (SY/P).

The bulk of the information in a large set can be retained when a large number of variables are reduced to a small set using the widely used PCA dimension reduction technique (Massay, 1965; Jolliffe, 1986). Thus, before beginning a hybridization program to create better hybrids in chickpeas, the current study used principal component analysis to assess chickpea germplasm in order to find and rank important traits and genotypes. A statistical tool for principal component analysis is the factoextra package in R Studio (Kassambara and Mundt, 2020).

Results and Discussion

According to the findings of the basic descriptive statistics for the ten quantitative variables, a significant amount of variation was observed among the chickpea genotypes under investigation (Table 2).

Principal component analysis is one basic non-parametric technique that can be used to extract relevant information from mixed datasets. Principal Component Analysis (PCA) is a popular technique for dimension reduction, as noted by Massay (1965) and Jolliffe (2002). It successfully reduces a sizable collection of variables into a more manageable set while preserving the majority of the information found in the original data.

The current study aimed to assess chickpea genotypes to pinpoint and rank significant traits and genotypes using principal component analysis (PCA) before starting a hybridization program to create improved chickpea crosses. A statistical technique called principal component analysis uses an orthogonal transformation to convert a collection of observations of possibly correlated variables into principal components, which are sets of values of linearly uncorrelated variables. There are as many primary components as there are original variables, or fewer. Each consecutive component in this transformation has the highest variance while being orthogonal to the preceding components, with the first principal component capturing the maximum variance (i.e., explaining as much variability in the data as feasible). An uncorrelated orthogonal basis set is formed by the resultant vectors. Since the principal components are eigenvectors of the symmetric covariance matrix, they are orthogonal (Kumar *et al.,* 2019).

In the present investigation, ten quantitative chickpea traits were subjected to PCA. Only three PCs out of ten had variability of roughly 63.97% and more than 1.0 eigenvalue (Table 3 and Fig. 1). Consequently, these three PCs received the attention they deserved in the current study. The genotypes for the characteristics under investigation were next in line, with PC1 explaining a total variation of 26.39% with an eigenvalue of 2.63. Table 2 lists the two PCs that contributed the most to the overall variation: PC 1 and PC 2. PC 1 explained the greatest percentage of overall variability in the collection of all variables, whereas the other components explained decreasing percentages of variation. PC 1 demonstrated the most variability at 26.39 %. This was followed by PC 2 (21.79%) with an eigenvalue of 2.17, and PC 3 (15.79%) with an eigenvalue of 1.57. The findings above indicate that yield-contributing features varied the most in PC1, followed by PC2 and PC3. PCA aims to identify the fewest components that account for the greatest amount of variability among all components. In addition, the germplasm was ranked according to the PC scores. Malik *et al.,* (2014) and Rajani *et al.,* (2020) had similar outcomes.

The results also indicated that in PC1 (fig. 2 and Table 3), the number of secondary branches per plant (0.437), number of primary branches per plant (0.426), seed yield per plant (0.433), 100 seed weight (0.330), days to 50% pod setting (0.327), days to 50% flowering (0.280), number of seeds per pod (0.221), days to maturity (0.207), and number of pods per plant (0.193) had the most significant positive values, whereas plant height (-0.128) showed a negative value. Days to 50% blooming (0.495), days to 50% pod setting (0.489), and days to maturity (0.465) showed the highest positive values in PC 2, but all other features showed negative loadings. Positive contributions of days to 50% pod set and days to 50% blooming (0.495) were found in the third component. Akande (2007); Ojo *et al.,* (2012); Miladinovic *et al.,* (2006); Shivwanshi and Babbar (2017) and Amrita *et al.,* (2014) corroborated these findings in chickpeas. According to their findings, the first PC was associated with characteristics that define production, such as the number of pods per plant, whereas the second PC was primarily dominated by phenological aspects.

More than one positive-scoring genotype was discovered in more PCs ICC 227, ICC 15510, ICC 107, ICC 2720, ICC 14778, ICC 8195, ICC 6816, ICC 867, ICC 19165, ICC 7867, ICC 440, ICC -16534, ICC -6816, ICC -12726, JG-14, BG3043, WR315, JAKI9218, PHULE G 405, JG74, CSJ-515, ICC -7877, ICC -3582, ICC -12324, ICC -6874, ICC -11764, ICC -11284, ICC -12307, ICC -8318, ICC -13628, ICC -10399, ICC -12299, ICC -4841, ICC 10341, ICC 16903, ICC 1533, ICC 6279, ICC -13523, ICC -13187, ICC -1357, Pusa JG-16, JG-24, Kundan, SamridhiJG-16, HC-5, GNG-2207 and GL-13001 (table 4 and fig 3).

Table.1 List of Genotypes used under this study

S. No	Genotype Name	S. No	Genotype Name	S. No	Genotype Name	S. No	Genotype Name	S. No	Genotype Name
1	ICC 4418	21	ICC 3218	41	ICC 8350	61	ICC -10399	81	ICC -3582
2	ICC 14669	22	ICC 2072	42	ICC 138	62	ICC -12299	82	Pusa JG-16
3	ICC 7819	23	ICC 2507	43	ICC 4495	63	ICC -4841	83	JG-24
4	ICC 11897	24	ICC 10673	44	ICC 14815	64	ICC -16534	84	Kundan
5	ICC 14446	25	ICC 16374	45	ICC 14778	65	ICC -6816	85	Samridhi
6	ICC 7323	26	ICC 19100	46	ICC 8195	66	ICC -8318	86	JG-14
7	ICC 762	27	ICC 6279	47	ICC 6816	67	ICC -11498	87	BG3043
8	ICC 10393	28	ICC 4491	48	ICC 10466	68	ICC -11284	88	WR315
9	ICC 16903	29	ICC 15435	49	ICC 867	69	ICC -12307	89	JAKI9218
10	ICC 1883	30	ICC 6294	50	ICC 19165	70	ICC -14687	90	PHULE G 405
11	ICC 6513	31	ICC 11121	51	ICC 7867	71	ICC -12328	91	JG74
12	ICC 1915	32	ICC 5845	52	ICC 440	72	ICC -1194	92	CSJ-515
13	ICC 6806	33	ICC 14831	53	ICC 1431	73	ICC -6874	93	JG-16
14	ICC 1533	34	ICC 227	54	ICC 19164	74	ICC -11764	94	HC-5
15	ICC 11378	35	ICC 15510	55	ICC - 4918	75	ICC -637	95	GNG-2207
16	ICC 1161	36	ICC 107	56	ICC -7819	76	ICC -13077	96	GL-13001
17	ICC 7326	37	ICC 2720	57	ICC -13523	77	ICC -12324		
18	ICC 56610	38	ICC 16795	58	ICC -13187	78	ICC -12726		
19	ICC 5434	39	ICC 26911	59	ICC -1205	79	ICC -1357		
20	ICC 9137	40	ICC 10341	60	ICC -13628	80	ICC -7877		

Table.2 Basic Descriptive Statistics of 10 yield-related traits

	DF 50%	DPS 50%	DM	PH	NPB	NSB	NPD/P	NSD/PD	100 SW	SY/P
Mean	75.97	87.35	115.52	34.90	5.25	13.76	52.07	1.69	14.79	13.38
Variance	7.01	10.69	62.78	45.99	2.84	12.52	188.87	0.21	9.57	27.80
St. dev.	2.65	3.27	7.92	6.78	1.68	3.54	13.74	0.46	3.09	5.27

Figure.1 Screen plot constructed based on thirteen principal component and their eigenvalues

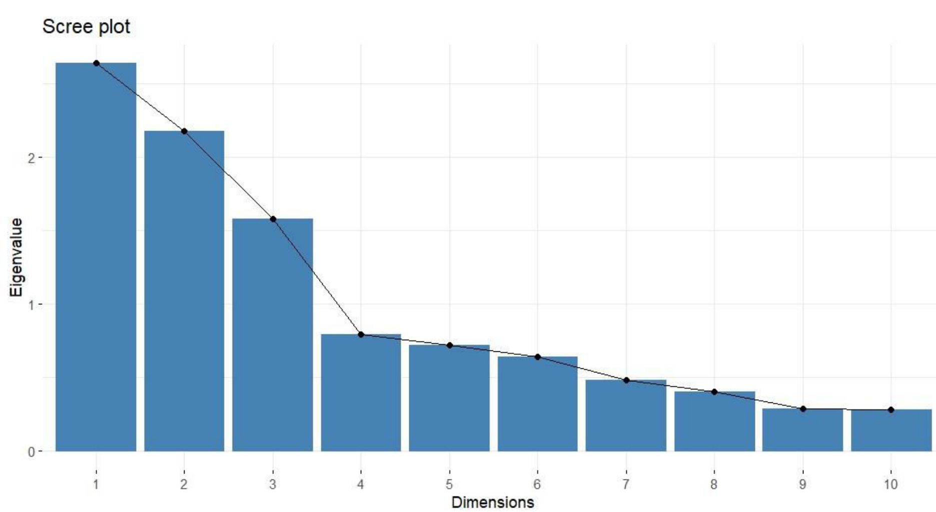


Table.3 Eigen value, Variability Contribution and Eigen vectors for the Principal Component Analysis in chickpea

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
DF 50%	0.280	0.495	0.005	0.009	-0.061	-0.151	-0.528	-0.114	0.423	0.423
DPS 50%	0.327	0.489	0.040	-0.024	0.090	0.034	-0.046	-0.241	-0.135	-0.751
DM	0.207	0.465	-0.259	0.151	0.308	-0.108	0.493	0.328	-0.298	0.324
PH	-0.128	-0.158	-0.588	-0.023	0.123	-0.667	-0.092	-0.363	-0.091	-0.066
NPB	0.426	-0.159	0.017	-0.482	-0.355	-0.304	-0.172	0.483	-0.278	-0.053
NSB	0.437	-0.117	-0.223	-0.064	-0.471	0.144	0.516	-0.380	0.283	0.094
NPD/P	0.193	-0.178	-0.510	0.575	-0.125	0.262	-0.284	0.362	0.085	-0.194
NSD/PD	0.221	-0.180	0.480	0.495	0.043	-0.548	0.197	0.120	0.267	-0.130
100 SW	0.330	-0.303	-0.102	-0.340	0.690	0.132	0.020	0.098	0.407	-0.065
SY/P	0.433	-0.283	0.187	0.222	0.193	0.143	-0.227	-0.397	-0.552	0.277
Eigenvalue	**2.639**	**2.179**	**1.579**	0.794	0.718	0.639	0.483	0.404	0.283	0.280
% of Variance	26.39%	21.79%	15.79%	7.94%	7.18%	6.39%	4.83%	4.04%	2.83%	2.80%
Cumulative % of Variance	26.39%	48.18%	63.98%	71.91%	79.10%	85.49%	90.32%	94.36%	97.20%	100.00%

Table.4 PCA score for 96 genotypes of Chickpea

S. No.	Genotype	PC 1	PC 2	PC 3	S. No.	Genotype	PC 1	PC 2	PC 3	S. No.	Genotype	PC 1	PC 2	PC 3	76	ICC - 13077	-2.614	0.896	0.006
1	**ICC 4418**	-1.295	-0.613	-0.560	26	**ICC 19100**	-0.380	-0.855	-0.147	51	**ICC 7867**	3.743	-1.119	-0.080	77	**ICC - 12324**	0.351	2.691	1.564
2	**ICC 14669**	-2.127	-0.386	-0.246	27	**ICC 6279**	-0.005	-1.028	1.133	52	**ICC 440**	2.110	-2.276	0.369	78	**ICC - 12726**	1.664	3.678	1.714
3	**ICC 7819**	-0.980	-0.712	-0.938	28	**ICC 4491**	0.398	-3.020	-1.282	53	**ICC 1431**	0.351	0.627	-0.671	79	**ICC - 1357**	-0.025	-0.491	4.866
4	**ICC 11897**	-0.656	-0.790	0.116	29	**ICC 15435**	-1.873	-1.340	-1.601	54	**ICC 19164**	0.743	-0.216	-0.449	80	**ICC - 7877**	-0.804	1.765	0.711
5	**ICC 14446**	-1.632	-1.075	-0.930	30	**ICC 6294**	0.047	-1.041	-0.017	55	**ICC - 4918**	-0.566	0.544	-1.051	81	**ICC - 3582**	0.135	1.858	0.222
6	**ICC 7323**	-0.707	-1.356	-1.018	31	**ICC 11121**	-0.837	-0.442	-2.657	56	**ICC - 7819**	-1.721	-1.135	-1.666	82	**Pusa JG-16**	0.860	-0.358	1.082
7	**ICC 762**	-2.307	0.160	-0.161	32	**ICC 5845**	-0.380	-0.615	-1.506	57	**ICC - 13523**	0.673	-0.648	1.466	83	**JG-24**	0.246	0.174	1.593
8	**ICC 10393**	-0.385	-0.921	-0.440	33	**ICC 14831**	0.034	0.001	-1.657	58	**ICC - 13187**	0.273	-1.142	1.419	84	**Kundan**	0.144	-0.664	1.453
9	**ICC 16903**	-0.6	-1.0	1.262	34	**ICC 227**	1.290	0.208	-1.1	59	**ICC - 1205**	-2.0	0.866	0.847	85	**Samridhi**	-0.2	-0.9	1.884

		90	33						39			07					35	14	
10	**ICC 1883**	-0.718	-0.366	-0.884	35	**ICC 15510**	2.345	0.664	-1.876	60	**ICC - 13628**	-1.395	2.018	-1.298	86	**JG-14**	1.415	-0.430	1.316
11	**ICC 6513**	-1.446	-0.114	-0.270	36	**ICC 107**	3.852	-0.429	-0.619	61	**ICC - 10399**	-1.480	3.174	-0.025	87	**BG3043**	3.487	0.117	0.155
12	**ICC 1915**	-1.573	0.210	-1.387	37	**ICC 2720**	2.814	-1.086	-0.294	62	**ICC - 12299**	-0.445	1.358	-0.145	88	**WR315**	4.435	-2.282	0.932
13	**ICC 6806**	-1.700	-0.173	0.638	38	**ICC 16795**	0.848	0.870	-2.028	63	**ICC - 4841**	-0.762	3.327	0.343	89	**JAKI 9218**	1.575	-0.495	-0.092
14	**ICC 1533**	-1.614	-1.498	1.631	39	**ICC 26911**	0.504	0.855	-1.456	64	**ICC - 16534**	2.091	3.158	0.841	90	**PHULE G 405**	1.379	1.032	-0.080
15	**ICC 11378**	-2.209	0.296	0.552	40	**ICC 10341**	0.861	1.092	-0.531	65	**ICC - 6816**	1.274	3.531	2.069	91	**JG74**	1.030	-0.356	0.446
16	**ICC 1161**	-0.050	-1.055	-0.072	41	**ICC 8350**	0.631	-0.799	-0.658	66	**ICC - 8318**	-2.137	3.948	-0.636	92	**CSJ-515**	1.563	1.258	2.001
17	**ICC 7326**	-1.260	-1.133	-0.471	42	**ICC 138**	-0.431	-0.201	-1.813	67	**ICC - 11498**	-1.953	0.772	0.892	93	**JG-16**	-1.582	-2.046	3.725
18	**ICC 56610**	-1.504	-0.040	-0.454	43	**ICC 4495**	0.634	0.042	-0.739	68	**ICC - 11284**	1.125	1.306	-0.686	94	**HC-5**	-3.558	-4.493	2.948
19	**ICC 5434**	-1.074	-1.362	-0.559	44	**ICC 14815**	0.730	0.845	-0.002	69	**ICC - 12307**	-0.841	1.863	-0.693	95	**GNG-2207**	-0.942	1.717	2.726
20	**ICC 9137**	-1.230	-0.329	-0.568	45	**ICC 14778**	4.386	-0.723	-0.486	70	**ICC - 14687**	-1.771	0.863	-1.298	96	**GL-13001**	0.570	-0.084	1.340
21	**ICC 3218**	-0.894	-1.361	-0.806	46	**ICC 8195**	1.878	-1.355	0.130	71	**ICC - 12328**	-1.233	-0.839	-0.084					
22	**ICC 2072**	-0.444	-2.317	-0.388	47	**ICC 6816**	3.981	-1.442	-0.235	72	**ICC - 1194**	0.329	2.990	-0.251					
23	**ICC 2507**	-1.454	-0.918	-0.802	48	**ICC 10466**	0.994	0.319	-1.400	73	**ICC - 6874**	-0.253	1.022	-1.089					
24	**ICC 10673**	-0.200	-0.399	0.012	49	**ICC 867**	2.083	-0.250	-0.225	74	**ICC - 11764**	-0.090	1.628	0.911					
25	**ICC 16374**	-0.392	-1.064	-0.522	50	**ICC 19165**	1.313	0.068	-1.341	75	**ICC - 637**	-2.331	-0.178	0.160					

Figure.2 Variable contribution of ten characters to Principal Component Analysis

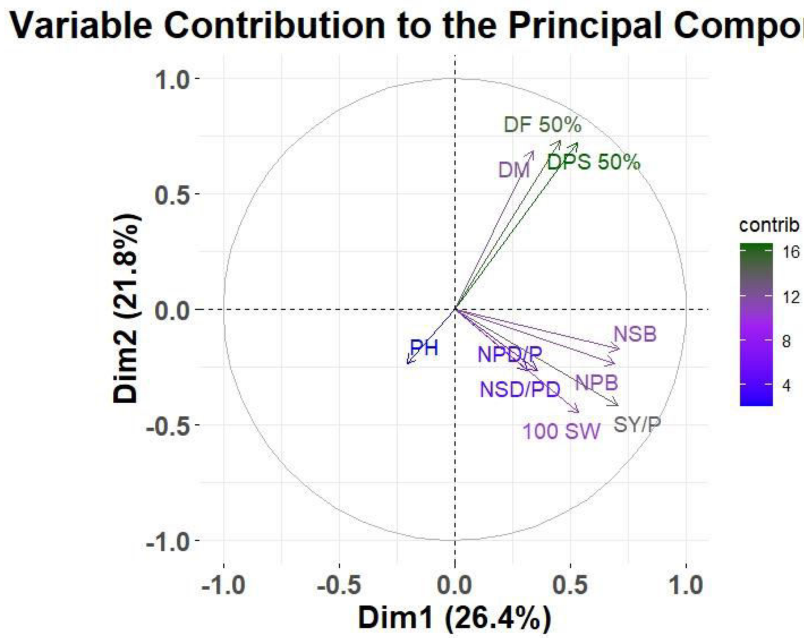


Figure.3 Individual Contribution to Principal Component Analysis

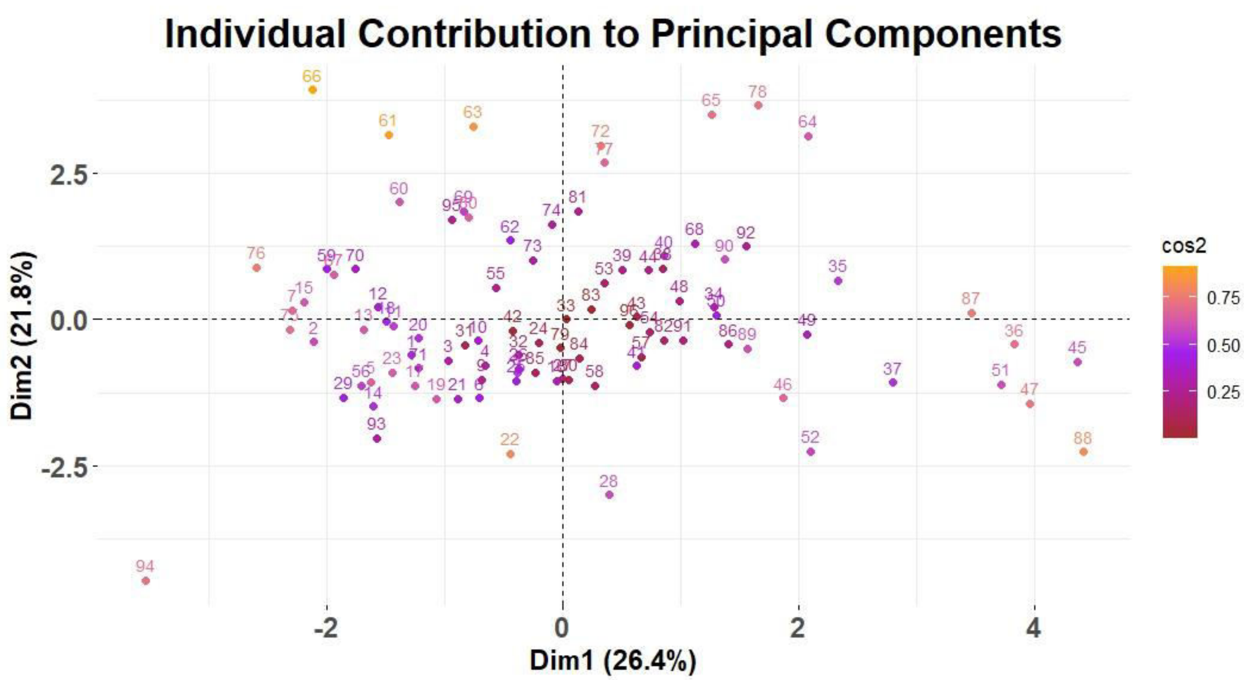
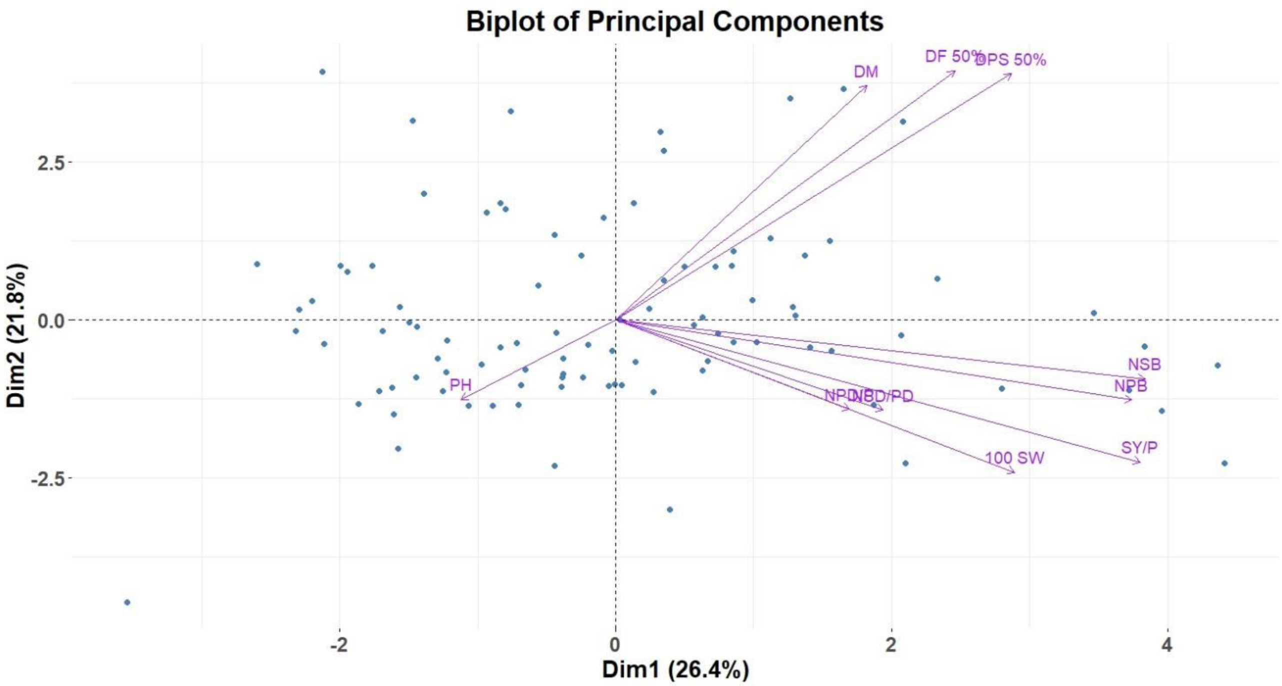


Figure.4 PCA Plot between 1st and 2nd component showing contribution of variability among



These genotypes can be used as ideotype breeding materials for selecting qualities linked to early maturity and seed yield, and they may also be used in breeding programs to increase seed yield (Rajani *et al.,* 2020; Jain *et al.,* 2023).

The distance of the variables to the PCs demonstrated their contributions to the genotypes (Fig. 4). The PCA biplot between PC1 and PC2 also showed that the most essential aspects contributing to genetic variability in the chickpea genotypes under study were the number of secondary branches per plant, seed yield per plant, number of primary branches per plant, 100 seed weight, days to 50% pod setting, days to 50% flowering, number of seeds per pod, days to maturity, and number of pods per plant.

The success of a breeding program aimed at improving chickpeas will depend more on the genotype selection made from the first three PCs (Mahmood *et al.,* 2018), and Malik *et al.,* (2014) published findings consistent with this study.

According to the PCA conducted in this study, the first three PCs—days to 50% pod setting, days to 50% flowering, days to maturity, and seed yield per plant—contributed 63.97% of the total divergence and traits. These three PCs also significantly contributed to the overall variation in the yield. Therefore, it is possible to simultaneously select yielding traits in chickpeas using PCs 1, 2, and 3. These qualities can be considered for the continued development and progress of chickpeas.

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Author Contributions

Deepesh Singh Koshle: Conceived the original idea and designed the model and wrote the manuscript.; Majjiga Revanth Kumar: Designed the model and the computational framework and analysed the data.; Chandragupt Maurya: Done the formal analysis; Nikhil Kumar: Validated the draft manuscript; Amit Kumar: Corrected the data sets; Niharika Yduvanshi: Investigated the entire framework of the manuscript; Shivam Tripathi: Conceptual idea; Utkarsh Tiwari: Reviewed; Neha Yadav: Draft manuscript; Dr. Shweta: Reviewed the original manuscript.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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